

SEQUENCE LISTING

<110> Klucher, Kevin M.
Sivakumar, Pallavur V.
Kindsvogel, Wayne R.
Henderson, Katherine E.

<120> METHODS FOR TREATING VIRAL INFECTION
USING IL-28 AND IL-29

<130> 02-24

<150> US 60/420,714
<151> 2002-10-23

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<151> 2003-04-18

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acc gtg act gga gca gtt cct gtc gcc agg ctc cac ggg gct ctc ccg 96
Thr Val Thr Gly Ala Val Pro Val Ala Arg Leu His Gly Ala Leu Pro
20 25 30

gat gca agg ggc tgc cac ata gcc cag ttc aag tcc ctg tct cca cag 144
Asp Ala Arg Gly Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln
35 40 45

gag ctg cag gcc ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt 192
Glu Leu Gln Ala Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu
50 55 60

ctg ctg aag gac tgc agg tgc cac tcc cgc ctc ttc ccc agg acc tgg Leu Leu Lys Asp Cys Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp 65 70 75 80	240
gac ctg agg cag ctg cag gtg agg gag cgc ccc atg gct ttg gag gct Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala 85 90 95	288
gag ctg gcc ctg acg ctg aag gtt ctg gag gcc acc gct gac act gac Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp 100 105 110	336
cca gcc ctg gtg gac gtc ttg gac cag ccc ctt cac acc ctg cac cat Pro Ala Leu Val Asp Val Leu Asp Gln Pro Leu His Thr Leu His His 115 120 125	384
atc ctc tcc cag ttc cgg gcc tgt gtg agt cgt cag ggc ctg ggc acc Ile Leu Ser Gln Phe Arg Ala Cys Val Ser Arg Gln Gly Leu Gly Thr 130 135 140	432
cag atc cag cct cag ccc acg gca ggg ccc agg acc cgg ggc cgc ctc Gln Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly Arg Leu 145 150 155 160	480
cac cat tgg ctg tac cgg ctc cag gag gcc cca aaa aag gag tcc cct His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Pro 165 170 175	528
ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc ctc ctc acg Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr 180 185 190	576
cga gac ctg aat tgt gtt gcc agt ggg gac ctg tgt gtc tga Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val *	618
195 200 205	

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Asp Ala Arg Gly Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln
35 40 45
Glu Leu Gln Ala Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu
50 55 60
Leu Leu Lys Asp Cys Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp
65 70 75 80
Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala
85 90 95
Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp
100 105 110
Pro Ala Leu Val Asp Val Leu Asp Gln Pro Leu His Thr Leu His His
115 120 125
Ile Leu Ser Gln Phe Arg Ala Cys Val Ser Arg Gln Gly Leu Gly Thr

130	135	140
Gln Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly Arg Leu		
145	150	155
His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Pro		160
165	170	175
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr		
180	185	190
Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val		
195	200	205

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gcc gtg gca ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag	96		
Ala Val Ala Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Gly Lys			
20	25	30	
ggc tgc cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg	144		
Gly Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala			
35	40	45	
agc ttc aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa	192		
Ser Phe Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys			
50	55	60	
aac tgg agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg	240		
Asn Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg			
65	70	75	80
ctt ctc cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc	288		
Leu Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala			
85	90	95	
ctg acg ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac	336		
Leu Thr Leu Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp			
100	105	110	
gtc cta gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc	384		
Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu			
115	120	125	
cag gcc tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cggtt ggc	432		
Gln Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly			
130	135	140	
cgc ctc cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag	480		

Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu			
145	150	155	160
tcc gct ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc			528
Ser Ala Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu			
165	170	175	
ctc acg cga gac ctc aaa tat gtg gcc gat ggg gac ctg tgt ctg aga			576
Leu Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg			
180	185	190	
acg tca acc cac cct gag tcc acc tga			603
Thr Ser Thr His Pro Glu Ser Thr *			
195	200		

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20	25	30	
Gly Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala			
35	40	45	
Ser Phe Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys			
50	55	60	
Asn Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg			
65	70	75	80
Leu Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala			
85	90	95	
Leu Thr Leu Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp			
100	105	110	
Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu			
115	120	125	
Gln Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly			
130	135	140	
Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu			
145	150	155	160
Ser Ala Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu			
165	170	175	
Leu Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg			
180	185	190	
Thr Ser Thr His Pro Glu Ser Thr			
195	200		

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acc gtg act gga gca gtt cct gtc gcc agg ctc cgc ggg gct ctc ccg 96
Thr Val Thr Gly Ala Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro
20 25 30

gat gca agg ggc tgc cac ata gcc cag ttc aag tcc ctg tct cca cag 144
Asp Ala Arg Gly Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln
35 40 45

gag ctg cag gcc ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt 192
Glu Leu Gln Ala Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu
50 55 60

ctg ctg aag gac tgc aag tgc cgc tcc cgc ctc ttc ccc agg acc tgg 240
Leu Leu Lys Asp Cys Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp
65 70 75 80

gac ctg agg cag ctg cag gtg agg gag cgc ccc gtg gct ttg gag gct 288
Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala
85 90 95

gag ctg gcc ctg acg ctg aag gtt ctg gag gcc acc gct gac act gac 336
Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp
100 105 110

cca gcc ctg ggg gat gtc ttg gac cag ccc ctt cac acc ctg cac cat 384
Pro Ala Leu Gly Asp Val Leu Asp Gln Pro Leu His Thr Leu His His
115 120 125

atc ctc tcc cag ctc cgg gcc tgt gtg agt cgt cag ggc ccg ggc acc 432
Ile Leu Ser Gln Leu Arg Ala Cys Val Ser Arg Gln Gly Pro Gly Thr
130 135 140

cag atc cag cct cag ccc acg gca ggg ccc agg acc cgg ggc cgc ctc 480
Gln Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly Arg Leu
145 150 155 160

cac cat tgg ctg cac cgg ctc cag gag gcc cca aaa aag gag tcc cct 528
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Pro
165 170 175

ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc ctc ctc acg 576
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
180 185 190

cga gac ctg aat tgt gtt gcc agc ggg gac ctg tgt gtc 615
Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
195 200 205

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20	25	30	
Asp Ala Arg Gly Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln			
35	40	45	
Glu Leu Gln Ala Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu			
50	55	60	
Leu Leu Lys Asp Cys Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp			
65	70	75	80
Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala			
85	90	95	
Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp			
100	105	110	
Pro Ala Leu Gly Asp Val Leu Asp Gln Pro Leu His Thr Leu His His			
115	120	125	
Ile Leu Ser Gln Leu Arg Ala Cys Val Ser Arg Gln Gly Pro Gly Thr			
130	135	140	
Gln Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly Arg Leu			
145	150	155	160
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Pro			
165	170	175	
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr			
180	185	190	
Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val			
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<220>

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			1			5						10	

ctc	ctc	ctg	ttg	cct	ctg	ctg	gcc	gca	gtg	ctg	aca	aga	acc	99
Leu	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Ala	Ala	Val	Leu	Thr	
15							20					25		

caa	gct	gac	cct	gtc	ccc	agg	gcc	acc	agg	ctc	cca	gtg	gaa	gca	aag	147
Gln	Ala	Asp	Pro	Val	Pro	Arg	Ala	Thr	Arg	Leu	Pro	Val	Glu	Ala	Lys	
30							35					40				

gat	tgc	cac	att	gct	cag	ttc	aag	tct	ctg	tcc	cca	aaa	gag	ctg	cag	195
Asp	Cys	His	Ile	Ala	Gln	Phe	Lys	Ser	Leu	Ser	Pro	Lys	Glu	Leu	Gln	
45							50					55				

gcc	ttc	aaa	aag	gcc	aag	gat	gcc	atc	gag	aag	agg	ctg	ctt	gag	aag	243
Ala	Phe	Lys	Ala	Lys	Asp	Ala	Ile	Glu	Lys	Arg	Leu	Leu	Glu	Lys		
60							65					70				

gac	ctg	agg	tgc	agt	tcc	cac	ctc	ttc	ccc	agg	gcc	tgg	gac	ctg	aag	291
Asp	Leu	Arg	Cys	Ser	Ser	His	Leu	Phe	Pro	Arg	Ala	Trp	Asp	Leu	Lys	
75							80					85		90		

cag	ctg	cag	gtc	caa	gag	cgc	ccc	aag	gcc	ttg	cag	gct	gag	gtg	gcc	339
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Gln	Leu	Gln	Val	Gln	Glu	Arg	Pro	Lys	Ala	Leu	Gln	Ala	Glu	Val	Ala	
95										100					105	
ctg	acc	ctg	aag	gtc	tgg	gag	aac	atg	act	gac	tca	gcc	ctg	gcc	acc	387
Leu	Thr	Leu	Lys	Val	Trp	Glu	Asn	Met	Thr	Asp	Ser	Ala	Leu	Ala	Thr	
110									115					120		
atc	ctg	ggc	cag	cct	ctt	cat	aca	ctg	agc	cac	att	cac	tcc	cag	ctg	435
Ile	Leu	Gly	Gln	Pro	Leu	His	Thr	Leu	Ser	His	Ile	His	Ser	Gln	Leu	
125									130				135			
cag	acc	tgt	aca	cag	ctt	cag	gcc	aca	gca	gag	ccc	agg	tcc	ccg	agc	483
Gln	Thr	Cys	Thr	Gln	Leu	Gln	Ala	Thr	Ala	Glu	Pro	Arg	Ser	Pro	Ser	
140									145				150			
cgc	cgc	ctc	tcc	cgc	tgg	ctg	cac	agg	ctc	cag	gag	gcc	cag	agc	aag	531
Arg	Arg	Leu	Ser	Arg	Trp	Leu	His	Arg	Leu	Gln	Glu	Ala	Gln	Ser	Lys	
155									160				165			170
gag	acc	cct	ggc	tgc	ctg	gag	gcc	tct	gtc	acc	tcc	aac	ctg	ttt	cgc	579
Glu	Thr	Pro	Gly	Cys	Leu	Glu	Ala	Ser	Val	Thr	Ser	Asn	Leu	Phe	Arg	
									175				180			185
ctg	ctc	acc	cgg	gac	ctc	aag	tgt	gtg	gcc	aat	gga	gac	cag	tgt	gtc	627
Leu	Leu	Thr	Arg	Asp	Leu	Lys	Cys	Val	Ala	Asn	Gly	Asp	Gln	Cys	Val	
									190				195			200
tga	cct															633
*																

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									20				25			30
Arg	Ala	Thr	Arg	Leu	Pro	Val	Glu	Ala	Lys	Asp	Cys	His	Ile	Ala	Gln	
									35				40			45
Phe	Lys	Ser	Leu	Ser	Pro	Lys	Glu	Leu	Gln	Ala	Phe	Lys	Lys	Ala	Lys	
									50				55			60
Asp	Ala	Ile	Glu	Lys	Arg	Leu	Leu	Glu	Lys	Asp	Leu	Arg	Cys	Ser	Ser	
									65				70			80
His	Leu	Phe	Pro	Arg	Ala	Trp	Asp	Leu	Lys	Gln	Leu	Gln	Val	Gln	Glu	
									85				90			95
Arg	Pro	Lys	Ala	Leu	Gln	Ala	Glu	Val	Ala	Leu	Thr	Leu	Lys	Val	Trp	
									100				105			110
Glu	Asn	Met	Thr	Asp	Ser	Ala	Leu	Ala	Thr	Ile	Leu	Gly	Gln	Pro	Leu	
									115				120			125
His	Thr	Leu	Ser	His	Ile	His	Ser	Gln	Leu	Gln	Thr	Cys	Thr	Gln	Leu	
									130				135			140
Gln	Ala	Thr	Ala	Glu	Pro	Arg	Ser	Pro	Ser	Arg	Arg	Leu	Ser	Arg	Trp	
									145				150			160
Leu	His	Arg	Leu	Gln	Glu	Ala	Gln	Ser	Lys	Glu	Thr	Pro	Gly	Cys	Leu	
									165				170			175
Glu	Ala	Ser	Val	Thr	Ser	Asn	Leu	Phe	Arg	Leu	Leu	Thr	Arg	Asp	Leu	
									180				185			190

Lys Cys Val Ala Asn Gly Asp Gln Cys Val
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1 5 10

ctc ctc ctg ctg ttg cct ctg ctg ctg gcc gca gtg ctg aca aga acc 99
 Leu Leu Leu Leu Leu Pro Leu Leu Leu Ala Ala Val Leu Thr Arg Thr
 15 20 25

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caa gct gac cct gtc ccc agg gcc acc agg ctc cca gtg gaa gca aag 147
Gln Ala Asp Pro Val Pro Arg Ala Thr Arg Leu Pro Val Glu Ala Lys
          30           35           40

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gat tgc cac att gct cag ttc aag tct ctg tcc cca aaa gag ctg cag	195	
Asp Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Lys Glu Leu Gln		
45	50	55

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gcc ttc aaa aag gcc aag ggt gcc atc gag aag agg ctg ctt gag aag 243
Ala Phe Lys Lys Ala Lys Gly Ala Ile Glu Lys Arg Leu Leu Glu Lys
       60           65           70

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gac atg agg tgc agt tcc cac ctc atc tcc agg gcc tgg gac ctg aag 291
Asp Met Arg Cys Ser Ser His Leu Ile Ser Arg Ala Trp Asp Leu Lys
    75           80           85           90

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cag ctg cag gtc caa gag cgccccc aag gcc ttgcag gct gag gtggcc 339
 Gln Leu Gln Val Gln Glu Arg Pro Lys Ala Leu Gln Ala Glu Val Ala
 95 100 105

ctg acc ctg aag gtc tgg gag aac ata aat gac tca gcc ctg acc acc 387
 Leu Thr Leu Lys Val Trp Glu Asn Ile Asn Asp Ser Ala Leu Thr Thr
 110 115 120

atc ctg ggc cag cct ctt cat aca ctg agc cac att cac tcc cag ctg 435
Ile Leu Gly Gln Pro Leu His Thr Leu Ser His Ile His Ser Gln Leu
125 130 135

cag acc tgt aca cag ctt cag gcc aca gca gag ccc aag ccc ccg agt	483
Gln Thr Cys Thr Gln Leu Gln Ala Thr Ala Glu Pro Lys Pro Pro Ser	
140 145 150	

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cgc cgc ctc tcc cgc tgg ctg cac agg ctc cag gag gcc cag agc aag      531
Arg Arg Leu Ser Arg Trp Leu His Arg Leu Gln Glu Ala Gln Ser Lys
155           160           165           170

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gag act cct ggc tgc ctg gag gac tct gtc acc tcc aac ctg ttt caa 579
 Glu Thr Pro Gly Cys Leu Glu Asp Ser Val Thr Ser Asn Leu Phe Gln
 175 180 185

ctg ctc ctc cgg gac ctc aag tgt gtg gcc agt gga gac cag tgc tgc	627
Leu Leu Leu Arg Asp Leu Lys Cys Val Ala Ser Gly Asp Gln Cys Val	
190	195
195	200

tga cc	632
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Arg Ala Thr Arg Leu Pro Val Glu Ala Lys Asp Cys His Ile Ala Gln	
35 40 45	
Phe Lys Ser Leu Ser Pro Lys Glu Leu Gln Ala Phe Lys Lys Ala Lys	
50 55 60	
Gly Ala Ile Glu Lys Arg Leu Leu Glu Lys Asp Met Arg Cys Ser Ser	
65 70 75 80	
His Leu Ile Ser Arg Ala Trp Asp Leu Lys Gln Leu Gln Val Gln Glu	
85 90 95	
Arg Pro Lys Ala Leu Gln Ala Glu Val Ala Leu Thr Leu Lys Val Trp	
100 105 110	
Glu Asn Ile Asn Asp Ser Ala Leu Thr Thr Ile Leu Gly Gln Pro Leu	
115 120 125	
His Thr Leu Ser His Ile His Ser Gln Leu Gln Thr Cys Thr Gln Leu	
130 135 140	
Gln Ala Thr Ala Glu Pro Lys Pro Pro Ser Arg Arg Leu Ser Arg Trp	
145 150 155 160	
Leu His Arg Leu Gln Glu Ala Gln Ser Lys Glu Thr Pro Gly Cys Leu	
165 170 175	
Glu Asp Ser Val Thr Ser Asn Leu Phe Gln Leu Leu Leu Arg Asp Leu	
180 185 190	
Lys Cys Val Ala Ser Gly Asp Gln Cys Val	
195 200	

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atg gcg ggg ccc gag cgc tgg ggc ccc ctg ctc ctg tgc ctg ctg cag	48
Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln	
1 5 10 15	

gcc gct cca ggg agg ccc cgt ctg gcc cct ccc cag aat gtg acg ctg	96
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Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu			
20	25	30	
ctc tcc cag aac ttc agc gtg tac ctg aca tgg ctc cca ggg ctt ggc			144
Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly			
35	40	45	
aac ccc cag gat gtg acc tat ttt gtg gcc tat cag agc tct ccc acc			192
Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr			
50	55	60	
cgt aga cgg tgg cgc gaa gtg gaa gag tgt gcg gga acc aag gag ctg			240
Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu			
65	70	75	80
cta tgt tct atg atg tgc ctg aag aaa cag gac ctg tac aac aag ttc			288
Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe			
85	90	95	
aag gga cgc gtg cgg acg gtt tct ccc agc tcc aag tcc ccc tgg gtg			336
Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val			
100	105	110	
gag tcc gaa tac ctg gat tac ctt ttt gaa gtg gag ccg gcc cca cct			384
Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro			
115	120	125	
gtc ctg gtg ctc acc cag acg gag atc ctg agt gcc aat gcc acg			432
Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr			
130	135	140	
tac cag ctg ccc ccc tgc atg ccc cca ctg gat ctg aag tat gag gtg			480
Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val			
145	150	155	160
gca ttc tgg aag gag ggg gcc gga aac aag acc cta ttt cca gtc act			528
Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Thr Leu Phe Pro Val Thr			
165	170	175	
ccc cat ggc cag cca gtc cag atc act ctc cag cca gct gcc agc gaa			576
Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu			
180	185	190	
cac cac tgc ctc agt gcc aga acc atc tac acg ttc agt gtc ccg aaa			624
His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro Lys			
195	200	205	
tac agc aag ttc tct aag ccc acc tgc ttc ttg ctg gag gtc cca gaa			672
Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro Glu			
210	215	220	
gcc aac tgg gct ttc ctg gtg ctg cca tcg ctt ctg ata ctg ctg tta			720
Ala Asn Trp Ala Phe Leu Val Leu Pro Ser Leu Leu Ile Leu Leu Leu			
225	230	235	240
gta att gcc gca ggg ggt gtg atc tgg aag acc ctc atg ggg aac ccc			768
Val Ile Ala Ala Gly Gly Val Ile Trp Lys Thr Leu Met Gly Asn Pro			
245	250	255	
tgg ttt cag cgg gca aag atg cca cgg gcc ctg gac ttt tct gga cac			816
Trp Phe Gln Arg Ala Lys Met Pro Arg Ala Leu Asp Phe Ser Gly His			
260	265	270	

aca cac cct gtg gca acc ttt cag ccc agc aga cca gag tcc gtg aat		864	
Thr His Pro Val Ala Thr Phe Gln Pro Ser Arg Pro Glu Ser Val Asn			
275	280	285	
gac ttg ttc ctc tgt ccc caa aag gaa ctg acc aga ggg gtc agg ccg		912	
Asp Leu Phe Leu Cys Pro Gln Lys Glu Leu Thr Arg Gly Val Arg Pro			
290	295	300	
acg cct cga gtc agg gcc cca gcc acc caa cag aca aga tgg aag aag		960	
Thr Pro Arg Val Arg Ala Pro Ala Thr Gln Gln Thr Arg Trp Lys Lys			
305	310	315	320
gac ctt gca gag gac gaa gag gag gat gag gag gac aca gaa gat		1008	
Asp Leu Ala Glu Asp Glu Glu Glu Asp Glu Glu Asp Thr Glu Asp			
325	330	335	
ggc gtc agc ttc cag ccc tac att gaa cca cct tct ttc ctg ggg caa		1056	
Gly Val Ser Phe Gln Pro Tyr Ile Glu Pro Pro Ser Phe Leu Gly Gln			
340	345	350	
gag cac cag gct cca ggg cac tcg gag gct ggt ggg gtg gac tca ggg		1104	
Glu His Gln Ala Pro Gly His Ser Glu Ala Gly Gly Val Asp Ser Gly			
355	360	365	
agg ccc agg gct cct ctg gtc cca agc gaa ggc tcc tct gct tgg gat		1152	
Arg Pro Arg Ala Pro Leu Val Pro Ser Glu Gly Ser Ser Ala Trp Asp			
370	375	380	
tct tca gac aga agc tgg gcc agc act gtg gac tcc tcc tgg gac agg		1200	
Ser Ser Asp Arg Ser Trp Ala Ser Thr Val Asp Ser Ser Trp Asp Arg			
385	390	395	400
gct ggg tcc tct ggc tat ttg gct gag aag ggg cca ggc caa ggg ccg		1248	
Ala Gly Ser Ser Gly Tyr Leu Ala Glu Lys Gly Pro Gly Gln Gly Pro			
405	410	415	
ggt ggg gat ggg cac caa gaa tct ctc cca cca cct gaa ttc tcc aag		1296	
Gly Gly Asp Gly His Gln Glu Ser Leu Pro Pro Glu Phe Ser Lys			
420	425	430	
gac tcg ggt ttc ctg gaa gag ctc cca gaa gat aac ctc tcc tcc tgg		1344	
Asp Ser Gly Phe Leu Glu Glu Leu Pro Glu Asp Asn Leu Ser Ser Trp			
435	440	445	
gcc acc tgg ggc acc tta cca ccg gag ccg aat ctg gtc cct ggg gga		1392	
Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Asn Leu Val Pro Gly Gly			
450	455	460	
ccc cca gtt tct ctt cag aca ctg acc ttc tgc tgg gaa agc agc cct		1440	
Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu Ser Ser Pro			
465	470	475	480
gag gag gaa gag gag gcg agg gaa tca gaa att gag gac agc gat gcg		1488	
Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp Ser Asp Ala			
485	490	495	
ggc agc tgg ggg gct gag agc acc cag agg acc gag gac agg ggc ccg		1536	
Gly Ser Trp Gly Ala Glu Ser Thr Gln Arg Thr Glu Asp Arg Gly Arg			
500	505	510	
aca ttg ggg cat tac atg gcc agg tga		1563	

Thr Leu Gly His Tyr Met Ala Arg *
 515 520

<210> 12
<211> 520
<212> PRT
<213> Homo sapiens

<400> 12
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 20 25 30
Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly
 35 40 45
Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr
 50 55 60
Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu
 65 70 75 80
Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe
 85 90 95
Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val
 100 105 110
Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro
 115 120 125
Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr
 130 135 140
Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val
 145 150 155 160
Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Thr Leu Phe Pro Val Thr
 165 170 175
Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu
 180 185 190
His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro Lys
 195 200 205
Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro Glu
 210 215 220
Ala Asn Trp Ala Phe Leu Val Leu Pro Ser Leu Leu Ile Leu Leu Leu
 225 230 235 240
Val Ile Ala Ala Gly Gly Val Ile Trp Lys Thr Leu Met Gly Asn Pro
 245 250 255
Trp Phe Gln Arg Ala Lys Met Pro Arg Ala Leu Asp Phe Ser Gly His
 260 265 270
Thr His Pro Val Ala Thr Phe Gln Pro Ser Arg Pro Glu Ser Val Asn
 275 280 285
Asp Leu Phe Leu Cys Pro Gln Lys Glu Leu Thr Arg Gly Val Arg Pro
 290 295 300
Thr Pro Arg Val Arg Ala Pro Ala Thr Gln Gln Thr Arg Trp Lys Lys
 305 310 315 320
Asp Leu Ala Glu Asp Glu Glu Glu Asp Glu Glu Asp Thr Glu Asp
 325 330 335
Gly Val Ser Phe Gln Pro Tyr Ile Glu Pro Pro Ser Phe Leu Gly Gln
 340 345 350
Glu His Gln Ala Pro Gly His Ser Glu Ala Gly Gly Val Asp Ser Gly
 355 360 365
Arg Pro Arg Ala Pro Leu Val Pro Ser Glu Gly Ser Ser Ala Trp Asp
 370 375 380
Ser Ser Asp Arg Ser Trp Ala Ser Thr Val Asp Ser Ser Trp Asp Arg
 385 390 395 400
Ala Gly Ser Ser Gly Tyr Leu Ala Glu Lys Gly Pro Gly Gln Gly Pro
 405 410 415

Gly Gly Asp Gly His Gln Glu Ser Leu Pro Pro Pro Glu Phe Ser Lys
 420 425 430
 Asp Ser Gly Phe Leu Glu Glu Leu Pro Glu Asp Asn Leu Ser Ser Trp
 435 440 445
 Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Asn Leu Val Pro Gly Gly
 450 455 460
 Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu Ser Ser Pro
 465 470 475 480
 Glu Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp Ser Asp Ala
 485 490 495
 Gly Ser Trp Gly Ala Glu Ser Thr Gln Arg Thr Glu Asp Arg Gly Arg
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 Thr Leu Gly His Tyr Met Ala Arg
 515 520

<210> 13
 <211> 1476
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1476)

<221> misc_feature
 <222> (0)...(0)
 <223> IL-28RA splice variant

<400> 13

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Met	Ala	Gly	Pro	Glu	Arg	Trp	Gly	Pro	Leu	Leu	Leu	Cys	Leu	Leu	Gln		
1			5						10					15			

gcc	gct	cca	ggg	agg	ccc	cgt	ctg	gcc	cct	ccc	cag	aat	gtg	acg	ctg		96
Ala	Ala	Pro	Gly	Arg	Pro	Arg	Leu	Ala	Pro	Pro	Gln	Asn	Val	Thr	Leu		
20				25								30					

ctc	tcc	cag	aac	ttc	agc	gtg	tac	ctg	aca	tgg	ctc	cca	ggg	ctt	ggc		144
Leu	Ser	Gln	Asn	Phe	Ser	Val	Tyr	Leu	Thr	Trp	Leu	Pro	Gly	Leu	Gly		
35			40									45					

aac	ccc	cag	gat	gtg	acc	tat	ttt	gtg	gcc	tat	cag	agc	tct	ccc	acc		192
Asn	Pro	Gln	Asp	Val	Thr	Tyr	Phe	Val	Ala	Tyr	Gln	Ser	Ser	Pro	Thr		
50			55								60						

cgt	aga	cg	tgg	cgc	gaa	gtg	gaa	gag	tgt	g	cc	acc	aag	gag	ctg		240
Arg	Arg	Arg	Trp	Arg	Glu	Val	Glu	Glu	Cys	Ala	Gly	Thr	Lys	Glu	Leu		
65				70					75				80				

cta	tgt	tct	atg	atg	tgc	ctg	aag	aaa	cag	gac	ctg	tac	aac	aag	ttc		288
Leu	Cys	Ser	Met	Met	Cys	Leu	Lys	Lys	Gln	Asp	Leu	Tyr	Asn	Lys	Phe		
85				90									95				

aag	gga	cgc	gtg	cg	ac	gt	tt	cc	ac	tc	aa	tc	cc	tt	gt		336
Lys	Gly	Arg	Val	Arg	Thr	Val	Ser	Pro	Ser	Ser	Lys	Ser	Pro	Trp	Val		
100				105							110						

gag	tcc	gaa	tac	ctg	gat	tac	ctt	ttt	gaa	gtg	gag	ccg	gcc	cca	cct		384
Glu	Ser	Glu	Tyr	Leu	Asp	Tyr	Leu	Phe	Glu	Val	Glu	Pro	Ala	Pro	Pro		
115				120							125						

gtc ctg gtg ctc acc cag acg gag gag atc ctg agt gcc aat gcc acg	432
Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr	
130 135 140	
tac cag ctg ccc ccc tgc atg ccc cca ctg ttt ctg aag tat gag gtg	480
Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Phe Leu Lys Tyr Glu Val	
145 150 155 160	
gca ttt tgg ggg ggg ggg gcc gga acc aag acc cta ttt cca gtc act	528
Ala Phe Trp Gly Gly Ala Gly Thr Lys Thr Leu Phe Pro Val Thr	
165 170 175	
ccc cat ggc cag cca gtc cag atc act ctc cag cca gct gcc agc gaa	576
Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu	
180 185 190	
cac cac tgc ctc agt gcc aga acc atc tac acg ttc agt gtc ccg aaa	624
His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro Lys	
195 200 205	
tac agc aag ttc tct aag ccc acc tgc ttc ttg ctg gag gtc cca gaa	672
Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro Glu	
210 215 220	
gcc aac tgg gct ttc ctg gtg ctc tcg cca tcg ctt ctg ata ctg ctg tta	720
Ala Asn Trp Ala Phe Leu Val Leu Pro Ser Leu Leu Ile Leu Leu Leu	
225 230 235 240	
gta att gcc gca ggg ggt gtg atc tgg aag acc ctc atg ggg aac ccc	768
Val Ile Ala Ala Gly Gly Val Ile Trp Lys Thr Leu Met Gly Asn Pro	
245 250 255	
tgg ttt cag cgg gca aag atg cca cgg gcc ctg gaa ctg acc aga ggg	816
Trp Phe Gln Arg Ala Lys Met Pro Arg Ala Leu Glu Leu Thr Arg Gly	
260 265 270	
gtc agg ccg acg cct cga gtc agg gcc cca gcc acc caa cag aca aga	864
Val Arg Pro Thr Pro Arg Val Arg Ala Pro Ala Thr Gln Gln Thr Arg	
275 280 285	
tgg aag aag gac ctt gca gag gac gaa gag gag gag gat gag gag gac	912
Trp Lys Lys Asp Leu Ala Glu Asp Glu Glu Glu Asp Glu Glu Asp	
290 295 300	
aca gaa gat ggc gtc agc ttc cag ccc tac att gaa cca cct tct ttc	960
Thr Glu Asp Gly Val Ser Phe Gln Pro Tyr Ile Glu Pro Pro Ser Phe	
305 310 315 320	
ctg ggg caa gag cac cag gct cca ggg cac tcg gag gct ggt ggg gtg	1008
Leu Gly Gln Glu His Gln Ala Pro Gly His Ser Glu Ala Gly Gly Val	
325 330 335	
gac tca ggg agg ccc agg gct cct ctg gtc cca agc gaa ggc tcc tct	1056
Asp Ser Gly Arg Pro Arg Ala Pro Leu Val Pro Ser Glu Gly Ser Ser	
340 345 350	
gct tgg gat tct tca gac aga agc tgg gcc agc act gtg gac tcc tcc	1104
Ala Trp Asp Ser Ser Asp Arg Ser Trp Ala Ser Thr Val Asp Ser Ser	
355 360 365	
tgg gac agg gct ggg tcc tct ggc tat ttg gct gag aag ggg cca ggc	1152
Trp Asp Arg Ala Gly Ser Ser Gly Tyr Leu Ala Glu Lys Gly Pro Gly	

370	375	380	
caa ggg ccg ggt ggg gat	ggg cac caa gaa tct ctc cca cca cct gaa		1200
Gln Gly Pro Gly Gly Asp	Gly His Gln Glu Ser Leu Pro Pro Pro Glu		
385	390	395	400
ttc tcc aag gac tcg ggt ttc ctg gaa gag ctc cca gaa gat aac ctc			1248
Phe Ser Lys Asp Ser Gly Phe Leu Glu Leu Pro Glu Asp Asn Leu			
405	410	415	
tcc tcc tgg gcc acc tgg ggc acc tta cca ccg gag ccg aat ctg gtc			1296
Ser Ser Trp Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Asn Leu Val			
420	425	430	
cct ggg gga ccc cca gtt tct ctt cag aca ctg acc ttc tgc tgg gaa			1344
Pro Gly Gly Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu			
435	440	445	
agc agc cct gag gag gaa gag gag gcg agg gaa tca gaa att gag gac			1392
Ser Ser Pro Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp			
450	455	460	
agc gat gcg ggc agc tgg ggg gct gag agc acc cag agg acc gag gac			1440
Ser Asp Ala Gly Ser Trp Gly Ala Glu Ser Thr Gln Arg Thr Glu Asp			
465	470	475	480
agg ggc cg aca ttg ggg cat tac atg gcc agg tga			1476
Arg Gly Arg Thr Leu Gly His Tyr Met Ala Arg *			
485	490		

<210> 14
<211> 491
<212> PRT
<213> Homo sapiens

<400> 14

Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln			
1	5	10	15
Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu			
20	25	30	
Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly			
35	40	45	
Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr			
50	55	60	
Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu			
65	70	75	80
Leu Cys Ser Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe			
85	90	95	
Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val			
100	105	110	
Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro			
115	120	125	
Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr			
130	135	140	
Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Phe Leu Lys Tyr Glu Val			
145	150	155	160
Ala Phe Trp Gly Gly Ala Gly Thr Lys Thr Leu Phe Pro Val Thr			
165	170	175	
Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu			
180	185	190	
His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro Lys			

	195	200	205
Tyr	Ser Lys Phe Ser Lys Pro	Thr Cys Phe Leu	Leu Glu Val Pro Glu
210	215	220	
Ala	Asn Trp Ala Phe Leu Val	Leu Pro Ser Leu	Leu Ile Leu Leu Leu
225	230	235	240
Val	Ile Ala Ala Gly Gly Val	Ile Trp Lys Thr	Leu Met Gly Asn Pro
	245	250	255
Trp	Phe Gln Arg Ala Lys Met Pro	Arg Ala Leu Glu	Leu Thr Arg Gly
	260	265	270
Val	Arg Pro Thr Pro Arg Val	Arg Ala Pro Ala	Thr Gln Gln Thr Arg
	275	280	285
Trp	Lys Lys Asp Leu Ala Glu	Asp Glu Glu	Glu Asp Glu Glu Asp
	290	295	300
Thr	Glu Asp Gly Val Ser	Phe Gln Pro Tyr	Ile Glu Pro Pro Ser Phe
305	310	315	320
Leu	Gly Gln Glu His Gln Ala	Pro Gly His	Ser Glu Ala Gly Gly Val
	325	330	335
Asp	Ser Gly Arg Pro Arg Ala Pro	Leu Val Pro Ser	Glu Gly Ser Ser
	340	345	350
Ala	Trp Asp Ser Ser Asp Arg Ser	Trp Ala Ser Thr	Val Asp Ser Ser
	355	360	365
Trp	Asp Arg Ala Gly Ser	Ser Gly Tyr	Leu Ala Glu Lys Gly Pro Gly
	370	375	380
Gln	Gly Pro Gly Gly Asp	Gly His Gln Glu	Ser Leu Pro Pro Pro Glu
385	390	395	400
Phe	Ser Lys Asp Ser Gly	Phe Leu Glu Glu	Leu Pro Glu Asp Asn Leu
	405	410	415
Ser	Ser Trp Ala Thr Trp Gly	Thr Leu Pro Pro Glu	Pro Asn Leu Val
	420	425	430
Pro	Gly Gly Pro Pro Val Ser	Leu Gln Thr Leu	Thr Phe Cys Trp Glu
	435	440	445
Ser	Ser Pro Glu Glu Glu	Glu Ala Arg Glu	Ser Glu Ile Glu Asp
	450	455	460
Ser	Asp Ala Gly Ser Trp Gly	Ala Glu Ser Thr	Gln Arg Thr Glu Asp
465	470	475	480
Arg	Gly Arg Thr Leu Gly His	Tyr Met Ala	Arg
	485	490	

<210> 15
<211> 674
<212> DNA
<213> *Homo sapiens*

<220>
<221> CDS
<222> (1) ... (636)

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<221> misc_feature
<222> (0)...(0)
<223> IL-28RA soluble variant
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<400> 15

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Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln
1 5 10 15

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gcc gct cca ggg agg ccc cgt ctg gcc cct ccc cag aat gtg acg ctg 96
Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu
          20           25           30

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ctc tcc caq aac ttc aqc qtq tac ctq aca tqg ctc cca qqq ctt qgc 144

Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly			
35	40	45	
aac ccc cag gat gtg acc tat ttt gtg gcc tat cag agc tct ccc acc			192
Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr			
50	55	60	
cgt aga cgg tgg cgc gaa gtg gaa gag tgt gcg gga acc aag gag ctg			240
Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu			
65	70	75	80
cta tgt tct atg atg tgc ctg aag aaa cag gac ctg tac aac aag ttc			288
Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe			
85	90	95	
aag gga cgc gtg cgg acg gtt tct ccc agc tcc aag tcc ccc tgg gtg			336
Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val			
100	105	110	
gag tcc gaa tac ctg gat tac ctt ttt gaa gtg gag ccg gcc cca cct			384
Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro			
115	120	125	
gtc ctg gtg ctc acc cag acg gag gag atc ctg agt gcc aat gcc acg			432
Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr			
130	135	140	
tac cag ctg ccc ccc tgc atg ccc cca ctg gat ctg aag tat gag gtg			480
Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val			
145	150	155	160
gca ttc tgg aag gag ggg gcc gga aac aag gtg gga agc tcc ttt cct			528
Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Val Gly Ser Ser Phe Pro			
165	170	175	
gcc ccc agg cta ggc ccg ctc ctc cac ccc ttc tta ctc agg ttc ttc			576
Ala Pro Arg Leu Gly Pro Leu Leu His Pro Phe Leu Leu Arg Phe Phe			
180	185	190	
tca ccc tcc cag cct gct cct gca ccc ctc ctc cag gaa gtc ttc cct			624
Ser Pro Ser Gln Pro Ala Pro Ala Pro Leu Leu Gln Glu Val Phe Pro			
195	200	205	
gta cac tcc tga cttctggcag tcagccctaa taaaatctga tcaaagta			674
Val His Ser *			
210			

<210> 16
<211> 211
<212> PRT
<213> Homo sapiens

<400> 16
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1 5 10 15
Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu
20 25 30
Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly
35 40 45
Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr
50 55 60

Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu
 65 70 75 80
 Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe
 85 90 95
 Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val
 100 105 110
 Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro
 115 120 125
 Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr
 130 135 140
 Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val
 145 150 155 160
 Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Val Gly Ser Ser Phe Pro
 165 170 175
 Ala Pro Arg Leu Gly Pro Leu Leu His Pro Phe Leu Leu Arg Phe Phe
 180 185 190
 Ser Pro Ser Gln Pro Ala Pro Ala Pro Leu Leu Gln Glu Val Phe Pro
 195 200 205
 Val His Ser
 210

<210> 17

<211> 734

<212> DNA

<213> Homo sapiens

<220>

<221> sig_peptide

<222> (53)....(127)

<221> mat_peptide

<222> (128)....(655)

<221> CDS

<222> (53)....(655)

<400> 17

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                                         Met Lys
                                         -25
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cta gac atg act ggg gac tgc acg cca gtg ctg gtg atg gcc gca 106
Leu Asp Met Thr Gly Asp Cys Thr Pro Val Leu Val Leu Met Ala Ala
-20           -15           -10
```

```
gtg ctg acc gtg act gga gca gtt cct gtc gcc agg ctc cac ggg gct 154
Val Leu Thr Val Thr Gly Ala Val Pro Val Ala Arg Leu His Gly Ala
-5             1               5
```

```
ctc ccg gat gca agg ggc tgc cac ata gcc cag ttc aag tcc ctg tct 202
Leu Pro Asp Ala Arg Gly Cys His Ile Ala Gln Phe Lys Ser Leu Ser
10            15            20            25
```

```
cca cag gag ctg cag gcc ttt aag agg gcc aaa gat gcc tta gaa gag 250
Pro Gln Glu Leu Gln Ala Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu
30            35            40
```

```
tcg ctt ctg ctg aag gac tgc agg tgc cac tcc cgc ctc ttc ccc agg 298
Ser Leu Leu Leu Lys Asp Cys Arg Cys His Ser Arg Leu Phe Pro Arg
45            50            55
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acc tgg gac ctg agg cag ctg cag gtg agg gag cgc ccc atg gct ttg	346
Thr Trp Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Met Ala Leu	
60 65 70	
gag gct gag ctg gcc ctg acg ctg aag gtt ctg gag gcc acc gct gac	394
Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr Ala Asp	
75 80 85	
act gac cca gcc ctg gtg gac gtc ttg gac cag ccc ctt cac acc ctg	442
Thr Asp Pro Ala Leu Val Asp Val Leu Asp Gln Pro Leu His Thr Leu	
90 95 100 105	
cac cat atc ctc tcc cag ttc cgg gcc tgt atc cag cct cag ccc acg	490
His His Ile Leu Ser Gln Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr	
110 115 120	
gca ggg ccc agg acc cgg ggc cgc ctc cac cat tgg ctg tac cgg ctc	538
Ala Gly Pro Arg Thr Arg Gly Arg Leu His His Trp Leu Tyr Arg Leu	
125 130 135	
cag gag gcc cca aaa aag gag tcc cct ggc tgc ctc gag gcc tct gtc	586
Gln Glu Ala Pro Lys Lys Glu Ser Pro Gly Cys Leu Glu Ala Ser Val	
140 145 150	
acc ttc aac ctc ttc cgc ctc acg cga gac ctg aat tgt gtt gcc	634
Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Asn Cys Val Ala	
155 160 165	
agt ggg gac ctg tgt gtc tga ccctccccacc agtcatgaa cctgagattt	685
Ser Gly Asp Leu Cys Val *	
170 175	
tatttataaa ttagccactt gtcttaattt attgccaccc agtcgctat	734
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<400> 18	
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-25 -20 -15 -10	
Ala Ala Val Leu Thr Val Thr Gly Ala Val Pro Val Ala Arg Leu His	
-5 1 5	
Gly Ala Leu Pro Asp Ala Arg Gly Cys His Ile Ala Gln Phe Lys Ser	
10 15 20	
Leu Ser Pro Gln Glu Leu Gln Ala Phe Lys Arg Ala Lys Asp Ala Leu	
25 30 35	
Glu Glu Ser Leu Leu Leu Lys Asp Cys Arg Cys His Ser Arg Leu Phe	
40 45 50 55	
Pro Arg Thr Trp Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Met	
60 65 70	
Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr	
75 80 85	
Ala Asp Thr Asp Pro Ala Leu Val Asp Val Leu Asp Gln Pro Leu His	
90 95 100	
Thr Leu His His Ile Leu Ser Gln Phe Arg Ala Cys Ile Gln Pro Gln	
105 110 115	

Pro	Thr	Ala	Gly	Pro	Arg	Thr	Arg	Gly	Arg	Leu	His	His	Trp	Leu	Tyr
120				125					130				135		
Arg	Leu	Gln	Glu	Ala	Pro	Lys	Lys	Glu	Ser	Pro	Gly	Cys	Leu	Glu	Ala
				140				145				150			
Ser	Val	Thr	Phe	Asn	Leu	Phe	Arg	Leu	Leu	Thr	Arg	Asp	Leu	Asn	Cys
				155				160				165			
Val	Ala	Ser	Gly	Asp	Leu	Cys	Val								
				170				175							

<210> 19
<211> 856
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> (98)...(154)

<221> mat_peptide
<222> (155)...(700)

<221> CDS
<222> (98)...(700)

<400> 19
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agagccatgc cgctgggaa gcagttgcga tttagcc atg gct gca gct tgg acc 115
Met Ala Ala Ala Trp Thr
-15

gtg gtg ctg gtg act ttg gtg cta ggc ttg gcc gtc gca ggc cct gtc 163
Val Val Leu Val Thr Leu Val Leu Gly Leu Ala Val Ala Gly Pro Val
-10 -5 1

ccc act tcc aag ccc acc aca act ggg aag ggc tgc cac att ggc agg 211
Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly Cys His Ile Gly Arg
5 10 15

tcc aaa tct ctg tca cca cag gag cta gcg agc ttc aag aag gcc agg 259
Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg
20 25 30 35

gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt tgc agc tct 307
Asp Ala Leu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser
40 45 50

cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag gtg agg gag 355
Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Gln Val Arg Glu
55 60 65

cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg aag gtc ctg 403
Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu
70 75 80

gag gcc gct ggc cca gcc ctg gag gac gtc cta gac cag ccc ctt 451
Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu
85 90 95

cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt atc cag cct 499
His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro
100 105 110 115

cag ccc aca gca ggg ccc agg ccc cg ^g ggc cgc ctc cac cac tgg ctg	547		
Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu			
120	125		
	130		
cac cg ^g ctc cag gag gcc ccc aaa aag gag tcc gct ggc tgc ctg gag	595		
His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu			
135	140		
	145		
gca tct gtc acc ttc aac ctc ttc cgc ctc acg cga gac ctc aaa	643		
Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys			
150	155		
	160		
tat gtg gcc gat ggg aac ctg tgt ctg aga acg tca acc cac cct gag	691		
Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser Thr His Pro Glu			
165	170		
	175		
tcc acc tga cacccccacac cttatttatg cgctgagccc tactccttcc	740		
Ser Thr *			
180			
ttaattttt tcctctcacc ctttatttat gaagctgcag ccctgactga gacataggc 800			
tgagttttt gtttacttt tatacattat gcacaaataa aacaacaagga attgga 856			
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Gly Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala			
15	20	25	
Ser Phe Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys			
30	35	40	45
Asn Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg			
50	55	60	
Leu Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala			
65	70	75	
Leu Thr Leu Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp			
80	85	90	
Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu			
95	100	105	
Gln Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly			
110	115	120	125
Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu			
130	135	140	
Ser Ala Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu			
145	150	155	
Leu Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg			
160	165	170	
Thr Ser Thr His Pro Glu Ser Thr			
175	180		

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<210> 21
<211> 734
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> (53)...(127)

<221> mat_peptide
<222> (128)...(655)

<221> CDS
<222> (53)...(655)

<400> 21
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                                         Met Lys
                                         -25

cta gac atg acc ggg gac tgc atg cca gtg ctg gtg ctg atg gcc gca 106
Leu Asp Met Thr Gly Asp Cys Met Pro Val Leu Val Leu Met Ala Ala
   -20                      -15                      -10

gtg ctg acc gtg act gga gca gtt cct gtc gcc agg ctc cgc ggg gct 154
Val Leu Thr Val Thr Gly Ala Val Pro Val Ala Arg Leu Arg Gly Ala
   -5                         1                         5

ctc ccg gat gca agg ggc tgc cac ata gcc cag ttc aag tcc ctg tct 202
Leu Pro Asp Ala Arg Gly Cys His Ile Ala Gln Phe Lys Ser Leu Ser
   10                        15                        20                        25

cca cag gag ctg cag gcc ttt aag agg gcc aaa gat gcc tta gaa gag 250
Pro Gln Glu Leu Gln Ala Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu
   30                        35                        40

tcg ctt ctg ctg aag gac tgc aag tgc cgc tcc cgc ctc ttc ccc agg 298
Ser Leu Leu Lys Asp Cys Lys Cys Arg Ser Arg Leu Phe Pro Arg
   45                        50                        55

acc tgg gac ctg agg cag ctg cag gtg agg gag cgc ccc gtg gct ttg 346
Thr Trp Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Val Ala Leu
   60                        65                        70

gag gct gag ctg gcc ctg acg ctg aag gtt ctg gag gcc acc gct gac 394
Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr Ala Asp
   75                        80                        85

act gac cca gcc ctg ggg gat gtc ttg gac cag ccc ctt cac acc ctg 442
Thr Asp Pro Ala Leu Gly Asp Val Leu Asp Gln Pro Leu His Thr Leu
   90                        95                       100                      105

cac cat atc ctc tcc cag ctc cgg gcc tgt atc cag cct cag ccc acg 490
His His Ile Leu Ser Gln Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr
   110                       115                      120

gca ggg ccc agg acc cgg ggc cgc ctc cac cat tgg ctg cac cgg ctc 538
Ala Gly Pro Arg Thr Arg Gly Arg Leu His His Trp Leu His Arg Leu
   125                       130                      135

cag gag gcc cca aaa aag gag tcc cct ggc tgc ctc gag gcc tct gtc 586
Gln Glu Ala Pro Lys Lys Glu Ser Pro Gly Cys Leu Glu Ala Ser Val

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140	145	150	
acc ttc aac ctc ttc cgc ctc acg cga gac ctg aat tgt gtt gcc			634
Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Asn Cys Val Ala			
155	160	165	
agc ggg gac ctg tgt gtc tga cccttccgcc agtcatgcaa cctgagattt			685
Ser Gly Asp Leu Cys Val *			
170	175		
tatttataaa ttagccactt ggcttaattt attgccaccc agtcgctat			734
<210> 22			
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<212> PRT			
<213> Homo sapiens			
<220>			
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<222> (1)...(25)			
<400> 22			
Met Lys Leu Asp Met Thr Gly Asp Cys Met Pro Val Leu Val Leu Met			
-25	-20	-15	-10
Ala Ala Val Leu Thr Val Thr Gly Ala Val Pro Val Ala Arg Leu Arg			
-5	1	5	
Gly Ala Leu Pro Asp Ala Arg Gly Cys His Ile Ala Gln Phe Lys Ser			
10	15	20	
Leu Ser Pro Gln Glu Leu Gln Ala Phe Lys Arg Ala Lys Asp Ala Leu			
25	30	35	
Glu Glu Ser Leu Leu Lys Asp Cys Lys Cys Arg Ser Arg Leu Phe			
40	45	50	55
Pro Arg Thr Trp Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Val			
60	65	70	
Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr			
75	80	85	
Ala Asp Thr Asp Pro Ala Leu Gly Asp Val Leu Asp Gln Pro Leu His			
90	95	100	
Thr Leu His His Ile Leu Ser Gln Leu Arg Ala Cys Ile Gln Pro Gln			
105	110	115	
Pro Thr Ala Gly Pro Arg Thr Arg Gly Arg Leu His His Trp Leu His			
120	125	130	135
Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Pro Gly Cys Leu Glu Ala			
140	145	150	
Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Asn Cys			
155	160	165	
Val Ala Ser Gly Asp Leu Cys Val			
170	175		
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<211> 528			
<212> DNA			
<213> Artificial Sequence			
<220>			
<223> IL-28A mutant C48S			
<221> CDS			
<222> (1)...(528)			
<400> 23			

gtt cct gtc gcc agg ctc cac ggg gct ctc ccg gat gca agg ggc tgc Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly Cys	48
1 5 10 15	
cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc ttt His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe	96
20 25 30	
aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac tcc Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Lys Asp Ser	144
35 40 45	
agg tgc cac tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag ctg Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu	192
50 55 60	
cag gtg agg gag cgc ccc atg gct ttg gag gct gag ctg gcc ctg acg Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu Thr	240
65 70 75 80	
ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg gtg gac Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val Asp	288
85 90 95	
gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag ttc Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Phe	336
100 105 110	
cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg ggc Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly	384
115 120 125	
cgc ctc cac cat tgg ctg tac cgg ctc cag gag gcc cca aaa aag gag Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu	432
130 135 140	
tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc ctc Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu	480
145 150 155 160	
ctc acg cga gac ctg aat tgt gtt gcc agt ggg gac ctg tgt gtc tga Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val *	528
165 170 175	

<210> 24
<211> 175
<212> PRT
<213> Artificial Sequence

<220>
<223> IL-28A mutant C48S

<400> 24
Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly Cys
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His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe
20 25 30
Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Lys Asp Ser
35 40 45
Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu

50	55	60
Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu Thr		
65	70	75
Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val Asp		
85	90	95
Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Phe		
100	105	110
Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly		
115	120	125
Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu		
130	135	140
Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu		
145	150	155
Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val		
165	170	175

<210> 25
<211> 531
<212> DNA
<213> Artificial Sequence

<220>
<223> met IL-28A mutant C49S

<221> CDS
<222> (1)...(531)

<400> 25		
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Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly		
1	5	10
		15
tgc cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc		96
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala		
20	25	30
ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac		144
Phe Lys Arg Ala Lys Asp Ala Leu Glu Ser Leu Leu Leu Lys Asp		
35	40	45
tcc agg tgc cac tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag		192
Ser Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln		
50	55	60
ctg cag gtg agg gag cgc ccc atg gct ttg gag gct gag ctg gcc ctg		240
Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu		
65	70	75
		80
acg ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg gtg		288
Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val		
85	90	95
gac gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag		336
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln		
100	105	110
ttc cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg		384
Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg		
115	120	125
ggc cgc ctc cac cat tgg ctg tac cgg ctc cag gag gcc cca aaa aag		432

Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys				
130	135	140		
gag tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc				480
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg				
145	150	155	160	
ctc ctc acg cga gac ctg aat tgt gtt gcc agt ggg gac ctg tgt gtc				528
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val				
165	170	175		
tga				531
*				

<210> 26
<211> 176
<212> PRT
<213> Artificial Sequence

<220>
<223> met IL-28A mutant C49S

<400> 26				
Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly				
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Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala				
20	25	30		
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Lys Asp				
35	40	45		
Ser Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln				
50	55	60		
Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu				
65	70	75	80	
Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val				
85	90	95		
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln				
100	105	110		
Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg				
115	120	125		
Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys				
130	135	140		
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg				
145	150	155	160	
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val				
165	170	175		

<210> 27
<211> 528
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-28A mutant C50S

<221> CDS
<222> (1)...(528)

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Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly Cys				
1	5	10	15	
cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc ttt				96
His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe				
20	25	30		
aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac tgc				144
Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Lys Asp Cys				
35	40	45		
agg tcc cac tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag ctg				192
Arg Ser His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu				
50	55	60		
cag gtg agg gag cgc ccc atg gct ttg gag gct gag ctg gcc ctg acg				240
Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu Thr				
65	70	75	80	
ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg gtg gac				288
Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val Asp				
85	90	95		
gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag ttc				336
Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Phe				
100	105	110		
cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg ggc				384
Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly				
115	120	125		
cgc ctc cac cat tgg ctg tac cgg ctc cag gag gcc cca aaa aag gag				432
Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu				
130	135	140		
tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc ctc				480
Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu				
145	150	155	160	
ctc acg cga gac ctg aat tgt gtt gcc agt ggg gac ctg tgt gtc tga				528
Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val *				
165	170	175		

<210> 28
<211> 175
<212> PRT
<213> Artificial Sequence

<220>
<223> IL-28A mutant C50S

<400> 28
Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly Cys
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His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe
20 25 30
Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Lys Asp Cys
35 40 45

Arg Ser His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu		
50	55	60
Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu Thr		
65	70	75
Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val Asp		
85	90	95
Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Phe		
100	105	110
Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly		
115	120	125
Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu		
130	135	140
Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu		
145	150	155
Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val		
165	170	175

<210> 29
<211> 531
<212> DNA
<213> Artificial Sequence

<220>
<223> met IL-28A mutant C51S

<221> CDS
<222> (1)...(531)

<400> 29		
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Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly		
1	5	10
		15
tgc cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc		96
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala		
20	25	30
ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac		144
Phe Lys Arg Ala Lys Asp Ala Leu Glu Ser Leu Leu Leu Lys Asp		
35	40	45
tgc agg tcc cac tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag		192
Cys Arg Ser His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln		
50	55	60
ctg cag gtg agg gag cgc ccc atg gct ttg gag gct gag ctg gcc ctg		240
Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu		
65	70	75
80		
acg ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg gtg		288
Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val		
85	90	95
gac gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag		336
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln		
100	105	110
tcc cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg		384
Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg		
115	120	125

ggc cgc ctc cac cat tgg ctg tac cg ^g ctc cag gag gcc cca aaa aag	432
Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys	
130 135 140	
gag tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc	480
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg	
145 150 155 160	
ctc ctc acg cga gac ctg aat tgt gtt gcc agt ggg gac ctg tgt gtc	528
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val	
165 170 175	
tga	531
*	

<210> 30
<211> 176
<212> PRT
<213> Artificial Sequence

<220>
<223> met IL-28A mutant C51S

<400> 30	
Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly	
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Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala	
20 25 30	
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp	
35 40 45	
Cys Arg Ser His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln	
50 55 60	
Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu	
65 70 75 80	
Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val	
85 90 95	
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln	
100 105 110	
Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg	
115 120 125	
Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys	
130 135 140	
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg	
145 150 155 160	
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val	
165 170 175	

<210> 31
<211> 546
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-29 mutant C171S

<221> CDS
<222> (1)...(546)

<400> 31

ggt ccg gtt ccg acc tct aaa cca acc acc act ggt aaa ggt tgc cac	48
Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly Cys His	
1 5 10 15	
atc ggt cgt ttc aaa tct ctg tct ccg cag gaa ctg gct tct ttc aaa	96
Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys	
20 25 30	
aaa gct cgt gac gct ctg gaa gaa tct ctg aaa ctg aaa aac tgg tct	144
Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser	
35 40 45	
tgc tct tct ccg gtt ttc ccg ggt aac tgg gat ctg cgt ctg cag	192
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln	
50 55 60	
gtt cgt gaa cgt ccg gtt gct ctg gaa gct gaa ctg gct ctg acc ctg	240
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu	
65 70 75 80	
aaa gtt ctg gaa gct gct gca ggt cct gct ctg gaa gat gtt ctg gat	288
Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp	
85 90 95	
cag ccg ctg cac act ctg cac cac atc ctg tct cag ctg cag gct tgc	336
Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys	
100 105 110	
att caa ccg caa ccg acc gct ggt ccg cgt ccg cgt ggt cgt ctg cac	384
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His	
115 120 125	
cac tgg ctg cat cgt ctg cag gaa gct ccg aaa aaa gaa tct gct ggt	432
His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly	
130 135 140	
tgc ctg gaa gct tct gtt acc ttc aac ctg ttc cgt ctg ctg acc cgt	480
Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg	
145 150 155 160	
gat ctg aaa tac gtt gct gat ggt aac ctg tct ctg cgt acc tct acc	528
Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Ser Leu Arg Thr Ser Thr	
165 170 175	
cat ccg gaa tct acc taa	546
His Pro Glu Ser Thr *	
180	

<210> 32
<211> 181
<212> PRT
<213> Artificial Sequence

<220>
<223> IL-29 mutant C171S

<400> 32
Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly Cys His
1 5 10 15
Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
20 25 30

Lys	Ala	Arg	Asp	Ala	Leu	Glu	Glu	Ser	Leu	Lys	Leu	Lys	Asn	Trp	Ser
35					40					45					
Cys	Ser	Ser	Pro	Val	Phe	Pro	Gly	Asn	Trp	Asp	Leu	Arg	Leu	Leu	Gln
50					55					60					
Val	Arg	Glu	Arg	Pro	Val	Ala	Leu	Glu	Ala	Glu	Leu	Ala	Leu	Thr	Leu
65					70					75					80
Lys	Val	Leu	Glu	Ala	Ala	Ala	Gly	Pro	Ala	Leu	Glu	Asp	Val	Leu	Asp
	85					90					95				
Gln	Pro	Leu	His	Thr	Leu	His	His	Ile	Leu	Ser	Gln	Leu	Gln	Ala	Cys
	100					105					110				
Ile	Gln	Pro	Gln	Pro	Thr	Ala	Gly	Pro	Arg	Pro	Arg	Gly	Arg	Leu	His
	115					120					125				
His	Trp	Leu	His	Arg	Leu	Gln	Glu	Ala	Pro	Lys	Lys	Glu	Ser	Ala	Gly
	130					135					140				
Cys	Leu	Glu	Ala	Ser	Val	Thr	Phe	Asn	Leu	Phe	Arg	Leu	Leu	Thr	Arg
145					150					155					160
Asp	Leu	Lys	Tyr	Val	Ala	Asp	Gly	Asn	Leu	Ser	Leu	Arg	Thr	Ser	Thr
	165					170					175				
His	Pro	Glu	Ser	Thr											
	180														

<210> 33
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> met IL-29 mutant C172S

<221> CDS
<222> (1)...(549)

<400> 33															
atg	ggt	ccg	gtt	ccg	acc	tct	aaa	cca	acc	acc	act	ggt	aaa	ggt	tgc
Met	Gly	Pro	Val	Pro	Thr	Ser	Lys	Pro	Thr	Thr	Thr	Gly	Lys	Gly	Cys
1					5				10				15		
cac	atc	ggt	cgt	ttc	aaa	tct	ctg	tct	ccg	cag	gaa	ctg	gct	tct	ttc
His	Ile	Gly	Arg	Phe	Lys	Ser	Leu	Ser	Pro	Gln	Glu	Leu	Ala	Ser	Phe
	20					25					30				96
aaa	aaa	gct	cgt	gac	gct	ctg	gaa	gaa	tct	ctg	aaa	ctg	aaa	aac	tgg
Lys	Lys	Ala	Arg	Asp	Ala	Leu	Glu	Glu	Ser	Leu	Lys	Leu	Lys	Asn	Trp
	35					40					45				
tct	tgc	tct	tct	ccg	gtt	ttc	ccg	ggt	aac	tgg	gat	ctg	cgt	ctg	ctg
Ser	Cys	Ser	Ser	Pro	Val	Phe	Pro	Gly	Asn	Trp	Asp	Leu	Arg	Leu	Leu
	50					55					60				
cag	gtt	cgt	gaa	cgt	ccg	gtt	gct	ctg	gaa	gct	ctg	gct	ctg	acc	
Gln	Val	Arg	Glu	Arg	Pro	Val	Ala	Leu	Glu	Leu	Ala	Glu	Leu	Ala	Leu
	65					70					75				80
ctg	aaa	gtt	ctg	gaa	gct	gca	ggt	cct	gct	ctg	gaa	gat	gtt	ctg	
Leu	Lys	Val	Leu	Glu	Ala	Ala	Gly	Pro	Ala	Leu	Glu	Asp	Val	Leu	
	85					90					95				288
gat	cag	ccg	ctg	cac	act	ctg	cac	cac	atc	ctg	tct	cag	ctg	cag	gct
Asp	Gln	Pro	Leu	His	Thr	Leu	His	His	Ile	Leu	Ser	Gln	Leu	Gln	Ala
	100					105					110				336

tgc att caa ccg caa ccg acc gct ggt ccg cgt ccg cgt ggt cgt ctg	384
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu	
115 120 125	
cac cac tgg ctg cat cgt ctg cag gaa gct ccg aaa aaa gaa tct gct	432
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala	
130 135 140	
ggc tgc ctg gaa gct tct gtt acc ttc aac ctg ttc cgt ctg ctg acc	480
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr	
145 150 155 160	
cgt gat ctg aaa tac gtt gct gat ggt aac ctg tct ctg cgt acc tct	528
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Ser Leu Arg Thr Ser	
165 170 175	
acc cat ccg gaa tct acc taa	549
Thr His Pro Glu Ser Thr *	
180	

<210> 34
<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<223> met IL-29 mutant C172S

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<400> 34
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys
      5          10          15
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
      20          25          30
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
      35          40          45
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
      50          55          60
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
      65          70          75          80
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
      85          90          95
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
      100         105         110
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
      115         120         125
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
      130         135         140
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
      145         150         155         160

```

Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Ser Leu Arg Thr Ser
 165 170 175
 Thr His Pro Glu Ser Thr
 180

```
<210> 35
<211> 531
<212> DNA
<213> Artificial Sequence
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<220>
<223> met IL-28A

<221> CDS
<222> (1) . . . (531)

```

<400> 35
atg gtt cct gtc gcc agg ctc cac ggg gct ctc ccg gat gca agg ggc 48
Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly
   1           5           10          15

```

```

tgc cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc 96
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
          20           25           30

```

```

ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac 144
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
          35           40           45

```

tgc agg tgc cac tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag	192
Cys Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln	
50 55 60	

ctg cag gtg agg gag cgc ccc atg gct ttg gag gct gag ctg gcc ctg 240
 Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu
 65 70 75 80

```

acg ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg gtg  288
Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val
                    85          90          95

```

```

gac gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag 336
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
          100           105           110

```

ttc cg^g gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cg^g 384
Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
115 120 125

```

ggc cgc ctc cac cat tgg ctg tac cgg ctc cag gag gcc cca aaa aag 432
Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
130          135          140

```

```

gag tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgcc 480
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
145           150           155           160

```

ctc ctc acg cga gac ctg aat tgt gtt gcc agt ggg gac ctg tgt gtc 528
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 165 170 175

tga
*

531

<210> 36
<211> 176
<212> PRT
<213> Artificial Sequence

<220>
<223> met IL-28A

<400> 36
Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly
1 5 10 15
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
20 25 30
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
35 40 45
Cys Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
50 55 60
Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu
65 70 75 80
Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val
85 90 95
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
100 105 110
Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
115 120 125
Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
130 135 140
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
145 150 155 160
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
165 170 175

<210> 37
<211> 621
<212> DNA
<213> Artificial Sequence

<220>
<223> met IL-29

<221> CDS
<222> (1)...(549)

<400> 37
atg ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc tgc 48
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly Cys
1 5 10 15
cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc 96
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
20 25 30
aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg 144
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
35 40 45

agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc	192
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu	
50 55 60	
cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg	240
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr	
65 70 75 80	
ctg aag gtc ctg gag gcc gct gtc cca gcc ctg gag gac gtc cta	288
Leu Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp Val Leu	
85 90 95	
gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc	336
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala	
100 105 110	
tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc	384
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu	
115 120 125	
cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct	432
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala	
130 135 140	
ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg	480
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr	
145 150 155 160	
cga gac ctc aaa tat gtg gcc gat ggg aac ctg tgt ctg aga acg tca	528
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser	
165 170 175	
acc cac cct gag tcc acc tga caccccacac cttatttatg cgctgagccc	579
Thr His Pro Glu Ser Thr *	
180	
taactcattcc ttaatttatt tcctctcacc cttatttat ga	621
<210> 38	
<211> 182	
<212> PRT	
<213> Artificial Sequence	
<220>	
<223> met IL-29	
<400> 38	
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys	
1 5 10 15	
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe	
20 25 30	
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp	
35 40 45	
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu	
50 55 60	
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr	
65 70 75 80	
Leu Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp Val Leu	
85 90 95	
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala	
100 105 110	

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<210> 39
<211> 531
<212> DNA
<213> Artificial Sequence
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<220>
<223> met IL-28B

<221> CDS
<222> (1) . . . (531)

<400> 39
atg gtt cct gtc gcc agg ctc cgc ggg gct ctc ccg gat gca agg ggc 48
Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly
1 5 10 15

```

tgc cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc 96
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
          20           25           30

```

ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac 144
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
 35 40 45

```
tgc aag tgc cgc tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag 192
Cys Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
      50          55          60
```

ctg cag gtg agg gag cgc ccc gtg gct ttg gag gct gag ctg gcc ctg 240
 Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
 65 70 75 80

acg ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg ggg 288
 Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Gly
 85 90 95

gat gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag 336
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
100 105 110

ctc cg^g g^cc t^gt a^tc c^ag c^ct c^ag c^{cc} a^cg g^ca g^{gg} c^{cc} a^{gg} a^cc c^{gg} 384
 Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
 115 120 125

```

ggc cgc ctc cac cat tgg ctg cac cgg ctc cag gag gcc cca aaa aag    432
Gly Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys
   130          135          140

```

gag tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc 480
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg

145	150	155	160	
ctc ctc acg cga gac ctg aat tgt gtt gcc agc ggg gac ctg tgt gtc				528
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val				
165	170	175		

tga
* 531

<210> 40
<211> 176
<212> PRT
<213> Artificial Sequence

<220>
<223> met IL-28B

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<400> 40
Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly
      1          5          10          15
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
      20         25         30
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
      35         40         45
Cys Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
      50         55         60
Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
      65         70         75         80
Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Gly
      85         90         95
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
      100        105        110
Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
      115        120        125
Gly Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys
      130        135        140
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
      145        150        155        160
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
      165        170        175

```